



CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/692,717

Filing Date: 10-20-00

Date Processed by STIC: 11-03-00

STIC Contact: Mark Spencer, 703-308-4212

Nature of Problem:

The CRF (was):

- ☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)
- ☐ Blank (no files on CRF) (see attached)
- ☐ Empty file (filename present, but no bytes in file) (see attached)
- ☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.
- ☐ Not saved in ASCII text
- ☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
- ☒ Did not contain a Sequence Listing. (see attached sample)
- ☐ Other: _____

**PLEASE USE THE CHECKER VERSION 3.0 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR DETAILS:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

09/692717

Protein Domain Table

Pfam	Prosite	Full Name	Description
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		Nitrilases / cyanide hydratase signatures	Nitrilases (EC 3.5.5.1) are enzymes that convert nitriles into their corresponding acids and ammonia. They are widespread in microbes as well as in plants where they convert indole-3-acetonitrile to the hormone indole-3-acetic acid. A conserved cysteine has been shown [1,2] to be essential for enzyme activity; it seems to be involved in a nucleophilic attack on the nitrile carbon atom. Cyanide hydratase (EC 4.2.1.66) converts HCN to formamide. In phytopathogenic fungi, it is used to avoid the toxic effect of cyanide released by wounded plants [3]. The sequence of cyanide hydrolase is evolutionary related to that of nitrilases. Yeast hypothetical proteins YIL164c and YIL165c also belong to this family. As signature patterns for these enzymes, two conserved regions were selected. The first is located in the N-terminal section while the second, which contains the active site cysteine, is located in the central section.
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Does Not Comply
Corrected Diskette Needed